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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/046,433

DATE: 01/28/2002
TIME: 13:44:34

p5

Input Set : **A:\PF511P1 seqlisting.txt**
Output Set: **N:\CRF3\01282002\J046433.raw**

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 3 <110> APPLICANT: Human Genome Sciences, Inc.
 5 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
 7 <130> FILE REFERENCE: PF511P1
 9 <140> CURRENT APPLICATION NUMBER: US/10/046,433
10 <141> CURRENT FILING DATE: 2002-01-16
12 <150> PRIOR APPLICATION NUMBER: 60/261,960
13 <151> PRIOR FILING DATE: 2001-01-17
15 <150> PRIOR APPLICATION NUMBER: 09/618,570
16 <151> PRIOR FILING DATE: 2000-07-14
18 <150> PRIOR APPLICATION NUMBER: 60/144,087
19 <151> PRIOR FILING DATE: 1999-07-16
21 <150> PRIOR APPLICATION NUMBER: 60/149,450
22 <151> PRIOR FILING DATE: 1999-07-18
24 <150> PRIOR APPLICATION NUMBER: 60/149,712
25 <151> PRIOR FILING DATE: 1999-08-20
27 <150> PRIOR APPLICATION NUMBER: 60/153,089
28 <151> PRIOR FILING DATE: 1999-09-10
30 <160> NUMBER OF SEQ ID NOS: 61
32 <170> SOFTWARE: PatentIn Ver. 2.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2554
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (31)..(2283)
43 <400> SEQUENCE: 1
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45                                     Met Asp Gln Ser Thr Gln Ala Cys
                                          1               5
46
48 gct ggt gag aaa cat tgc cat aac agg ggt ggc cta cac ttc aga atg   102
49 Ala Gly Glu Lys His Cys His Asn Arg Gly Gly Leu His Phe Arg Met
50          10              15              20
52 ctt ccc ctg caa acc tgg cac gta tgc aga caa gca ggg ctc ctc ttt   150
53 Leu Pro Leu Gln Thr Trp His Val Cys Arg Gln Ala Gly Leu Leu Phe
54    25              30              35              40
56 ctg caa act ttg ccc agc aac tct tat tca aat aaa gga gaa act tct   198
57 Leu Gln Thr Leu Pro Ser Asn Ser Tyr Ser Asn Lys Gly Glu Thr Ser
58                45              50              55
60 tgc cac cag tgt gac cct gac aaa tac tca gag aaa gga tct tct tcc   246
61 Cys His Gln Cys Asp Pro Asp Lys Tyr Ser Glu Lys Gly Ser Ser Ser
62             60              65              70
64 tgt aac gtg cgc cca gct tgc aca gac aaa gat tat ttc tac aca cac   294
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65 Cys Asn Val Arg Pro Ala Cys Thr Asp Lys Asp Tyr Phe Tyr Thr His
66           75                  80              85
68 acg gcc tgc gat gcc aac gga gag aca caa ctc atg tac aaa tgg gcc      342
69 Thr Ala Cys Asp Ala Asn Gly Glu Thr Gln Leu Met Tyr Lys Trp Ala
70      90                  95              100
72 aag ccg aaa atc tgt agc gag gac ctt gag ggg gca gtg aag ctg cct      390
73 Lys Pro Lys Ile Cys Ser Glu Asp Leu Glu Gly Ala Val Lys Leu Pro
74 105                 110                 115             120
76 gcc tct ggt gtg aag acc cac tgc cca ccc tgc aac cca ggc ttc ttc      438
77 Ala Ser Gly Val Lys Thr His Cys Pro Pro Cys Asn Pro Gly Phe Phe
78               125             130                 135
80 aaa acc aac aac agc acc tgc cag ccc tgc cca tat ggt tcc tac tcc      486
81 Lys Thr Asn Asn Ser Thr Cys Gln Pro Cys Pro Tyr Gly Ser Tyr Ser
82          140                 145                 150
84 aat ggc tca gac tgt acc cgc tgc cct gca ggg act gaa cct gct gtg      534
85 Asn Gly Ser Asp Cys Thr Arg Cys Pro Ala Gly Thr Glu Pro Ala Val
86          155             160                 165
88 gga ttt gaa tac aaa tgg tgg aac acg ctg ccc aca aac atg gaa acg      582
89 Gly Phe Glu Tyr Lys Trp Trp Asn Thr Leu Pro Thr Asn Met Glu Thr
90      170             175             180
92 acc gtt ctc agt ggg atc aac ttc gag tac aag ggc atg aca ggc tgg      630
93 Thr Val Leu Ser Gly Ile Asn Phe Glu Tyr Lys Gly Met Thr Gly Trp
94 185                 190                 195             200
96 gag gtg gct ggt gat cac att tac aca gct gct gga gcc tca gac aat      678
97 Glu Val Ala Gly Asp His Ile Tyr Thr Ala Ala Gly Ala Ser Asp Asn
98                  205             210                 215
100 gac ttc atg att ctc act ctg gtt gtg cca gga ttt aga cct ccg cag     726
101 Asp Phe Met Ile Leu Thr Leu Val Val Pro Gly Phe Arg Pro Pro Gln
102              220             225                 230
104 tcg gtg atg gca gac aca gag aat aaa gag gtg gcc aga atc aca ttt      774
105 Ser Val Met Ala Asp Thr Glu Asn Lys Glu Val Ala Arg Ile Thr Phe
106              235             240                 245
108 gtc ttt gag acc ctc tgt tct gtg aac tgt gag ctc tac ttc atg gtg      822
109 Val Phe Glu Thr Leu Cys Ser Val Asn Cys Glu Leu Tyr Phe Met Val
110     250             255                 260
112 ggt gtg aat tct agg acc aac act cct gtg gag acg tgg aaa ggt tcc      870
113 Gly Val Asn Ser Arg Thr Asn Thr Pro Val Glu Thr Trp Lys Gly Ser
114 265                 270                 275             280
116 aaa ggc aaa cag tcc tat acc tac atc att gag gag aac act acc acg      918
117 Lys Gly Lys Gln Ser Tyr Thr Tyr Ile Ile Glu Glu Asn Thr Thr Thr
118                  285             290                 295
120 agc ttc acc tgg gcc ttc cag agg acc act ttt cat gag gca agc agg      966
121 Ser Phe Thr Trp Ala Phe Gln Arg Thr Thr Phe His Glu Ala Ser Arg
122              300             305                 310
124 aag tac acc aat gac gtt gcc aag atc tac tcc atc aat gtc acc aat     1014
125 Lys Tyr Thr Asn Asp Val Ala Lys Ile Tyr Ser Ile Asn Val Thr Asn
126          315             320                 325
128 gtt atg aat ggc gtg gcc tcc tac tgc cgt ccc tgt gcc cta gaa gcc    1062
129 Val Met Asn Gly Val Ala Ser Tyr Cys Arg Pro Cys Ala Leu Glu Ala
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132 tct gat gtg ggc tcc tcc tgc acc tct tgt cct gct ggt tac tat att    1110
133 Ser Asp Val Gly Ser Ser Cys Thr Ser Cys Pro Ala Gly Tyr Tyr Ile
134 345                    350                  355                  360
136 gac cga gat tca gga acc tgc cac tcc tgc ccc cct aac aca att ctg    1158
137 Asp Arg Asp Ser Gly Thr Cys His Ser Cys Pro Pro Asn Thr Ile Leu
138                    365                  370                  375
140 aaa gcc cac cag cct tat ggt gtc cag gcc tgt gtg ccc tgt ggt cca    1206
141 Lys Ala His Gln Pro Tyr Gly Val Gln Ala Cys Val Pro Cys Gly Pro
142                    380                  385                  390
144 ggg acc aag aac aac aag atc cac tct ctg tgc tac aat gat tgc acc    1254
145 Gly Thr Lys Asn Asn Lys Ile His Ser Leu Cys Tyr Asn Asp Cys Thr
146          395                  400                  405
148 ttc tca cgc aac act cca acc agg act ttc aac tac aac ttc tcc gct    1302
149 Phe Ser Arg Asn Thr Pro Thr Arg Thr Phe Asn Tyr Asn Phe Ser Ala
150          410                  415                  420
152 ttg gca aac acc gtc act ctt gct gga ggg cca agc ttc act tcc aaa    1350
153 Leu Ala Asn Thr Val Thr Leu Ala Gly Gly Pro Ser Phe Thr Ser Lys
154 425                    430                  435                  440
156 ggg ttg aaa tac ttc cat cac ttt acc ctc agt ctc tgt gga aac cag    1398
157 Gly Leu Lys Tyr Phe His His Phe Thr Leu Ser Leu Cys Gly Asn Gln
158                    445                  450                  455
160 ggt agg aaa atg tct gtg tgc acc gac aat gtc act gac ctc cgg att    1446
161 Gly Arg Lys Met Ser Val Cys Thr Asp Asn Val Thr Asp Leu Arg Ile
162          460                  465                  470
164 cct gag ggt gag tca ggg ttc tcc aaa tct atc aca gcc tac gtc tgc    1494
165 Pro Glu Gly Glu Ser Gly Phe Ser Lys Ser Ile Thr Ala Tyr Val Cys
166          475                  480                  485
168 cag gca gtc atc atc ccc cca gag gtg aca ggc tac aag gcc ggg gtt    1542
169 Gln Ala Val Ile Ile Pro Pro Glu Val Thr Gly Tyr Lys Ala Gly Val
170      490                  495                  500
172 tcc tca cag cct gtc agc ctt gct gat cga ctt att ggg gtg aca aca    1590
173 Ser Ser Gln Pro Val Ser Leu Ala Asp Arg Leu Ile Gly Val Thr Thr
174 505                    510                  515                  520
176 gat atg act ctg gat gga atc acc tcc cca gct gaa ctt ttc cac ctg    1638
177 Asp Met Thr Leu Asp Gly Ile Thr Ser Pro Ala Glu Leu Phe His Leu
178                    525                  530                  535
180 gag tcc ttg gga ata ccg gac gtg atc ttc ttt tat agg tcc aat gat    1686
181 Glu Ser Leu Gly Ile Pro Asp Val Ile Phe Phe Tyr Arg Ser Asn Asp
182                    540                  545                  550
184 gtg acc cag tcc tgc agt tct ggg aga tca acc acc atc cgc gtc agg    1734
185 Val Thr Gln Ser Cys Ser Ser Gly Arg Ser Thr Thr Ile Arg Val Arg
186          555                  560                  565
188 tgc agt cca cag aaa act gtc cct gga agt ttg ctg ctg cca gga acg    1782
189 Cys Ser Pro Gln Lys Thr Val Pro Gly Ser Leu Leu Leu Pro Gly Thr
190      570                  575                  580
192 tgc tca gat ggg acc tgt gat ggc tgc aac ttc cac ttc ctg tgg gag    1830
193 Cys Ser Asp Gly Thr Cys Asp Gly Cys Asn Phe His Phe Leu Trp Glu
194 585                    590                  595                  600
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196 agc gcg gct gct tgc ccg ctc tgc tca gtg gct gac tac cat gct atc   1878
197 Ser Ala Ala Ala Cys Pro Leu Cys Ser Val Ala Asp Tyr His Ala Ile
198                 605             610             615
200 gtc agc agc tgt gtg gct ggg atc cag aag act act tac gtg tgg cga   1926
201 Val Ser Ser Cys Val Ala Gly Ile Gln Lys Thr Thr Tyr Val Trp Arg
202             620             625             630
204 gaa ccc aag cta tgc tct ggt ggc att tct ctg cct gag cag aga gtc   1974
205 Glu Pro Lys Leu Cys Ser Gly Gly Ile Ser Leu Pro Glu Gln Arg Val
206         635             640             645
208 acc atc tgc aaa acc ata gat ttc tgg ctg aaa gtg ggc atc tct gca   2022
209 Thr Ile Cys Lys Thr Ile Asp Phe Trp Leu Lys Val Gly Ile Ser Ala
210     650             655             660
212 ggc acc tgt act gcc atc ctg ctc acc gtc ttg acc tgc tac ttt tgg   2070
213 Gly Thr Cys Thr Ala Ile Leu Leu Thr Val Leu Thr Cys Tyr Phe Trp
214 665             670             675             680
216 aaa aag aat caa aaa cta gag tac aag tac tcc aag ctg gtg atg aat   2118
217 Lys Lys Asn Gln Lys Leu Glu Tyr Lys Tyr Ser Lys Leu Val Met Asn
218             685             690             695
220 gct act ctc aag gac tgt gac ctg cca gca gct gac agc tgc gcc atc   2166
221 Ala Thr Leu Lys Asp Cys Asp Leu Pro Ala Ala Asp Ser Cys Ala Ile
222         700             705             710
224 atg gaa ggc gag gat gta gag gac gac ctc atc ttt acc agc aag aat   2214
225 Met Glu Gly Glu Asp Val Glu Asp Asp Leu Ile Phe Thr Ser Lys Asn
226         715             720             725
228 cac tct ttg gga aga tca aat cat tta cct cca aga gga ctc ctg atg   2262
229 His Ser Leu Gly Arg Ser Asn His Leu Pro Pro Arg Gly Leu Leu Met
230     730             735             740
232 gat ttg act cag tgc cgc tga agacatcctc aggaggccca gacatggacc      2313
233 Asp Leu Thr Gln Cys Arg
234 745             750
236 tgtgagaggc actgcctgcc tcacctgcct cctcaccttg catagcacct ttgcaagcct 2373
238 gcggcgattt gggtgccagc atcctgcaac acccactgct ggaaatctct tcattgtggc 2433
240 cttatcagat gtttgaattt cagatctttt tttatagagt acccaaaccc tcctttctgc 2493
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248 <211> LENGTH: 750
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
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256 Arg Gly Gly Leu His Phe Arg Met Leu Pro Leu Gln Thr Trp His Val
257             20              25              30
259 Cys Arg Gln Ala Gly Leu Leu Phe Leu Gln Thr Leu Pro Ser Asn Ser
260         35              40              45
262 Tyr Ser Asn Lys Gly Glu Thr Ser Cys His Gln Cys Asp Pro Asp Lys
263     50              55              60
265 Tyr Ser Glu Lys Gly Ser Ser Ser Cys Asn Val Arg Pro Ala Cys Thr
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266  65                      70              75                  80
268  Asp Lys Asp Tyr Phe Tyr Thr His Thr Ala Cys Asp Ala Asn Gly Glu
269              85              90              95
271  Thr Gln Leu Met Tyr Lys Trp Ala Lys Pro Lys Ile Cys Ser Glu Asp
272          100             105             110
274  Leu Glu Gly Ala Val Lys Leu Pro Ala Ser Gly Val Lys Thr His Cys
275          115             120             125
277  Pro Pro Cys Asn Pro Gly Phe Phe Lys Thr Asn Asn Ser Thr Cys Gln
278      130             135             140
280  Pro Cys Pro Tyr Gly Ser Tyr Ser Asn Gly Ser Asp Cys Thr Arg Cys
281  145             150             155             160
283  Pro Ala Gly Thr Glu Pro Ala Val Gly Phe Glu Tyr Lys Trp Trp Asn
284              165             170             175
286  Thr Leu Pro Thr Asn Met Glu Thr Thr Val Leu Ser Gly Ile Asn Phe
287          180             185             190
289  Glu Tyr Lys Gly Met Thr Gly Trp Glu Val Ala Gly Asp His Ile Tyr
290          195             200             205
292  Thr Ala Ala Gly Ala Ser Asp Asn Asp Phe Met Ile Leu Thr Leu Val
293      210             215             220
295  Val Pro Gly Phe Arg Pro Pro Gln Ser Val Met Ala Asp Thr Glu Asn
296  225             230             235             240
298  Lys Glu Val Ala Arg Ile Thr Phe Val Phe Glu Thr Leu Cys Ser Val
299              245             250             255
301  Asn Cys Glu Leu Tyr Phe Met Val Gly Val Asn Ser Arg Thr Asn Thr
302          260             265             270
304  Pro Val Glu Thr Trp Lys Gly Ser Lys Gly Lys Gln Ser Tyr Thr Tyr
305          275             280             285
307  Ile Ile Glu Glu Asn Thr Thr Thr Ser Phe Thr Trp Ala Phe Gln Arg
308      290             295             300
310  Thr Thr Phe His Glu Ala Ser Arg Lys Tyr Thr Asn Asp Val Ala Lys
311  305             310             315             320
313  Ile Tyr Ser Ile Asn Val Thr Asn Val Met Asn Gly Val Ala Ser Tyr
314              325             330             335
316  Cys Arg Pro Cys Ala Leu Glu Ala Ser Asp Val Gly Ser Ser Cys Thr
317          340             345             350
319  Ser Cys Pro Ala Gly Tyr Tyr Ile Asp Arg Asp Ser Gly Thr Cys His
320          355             360             365
322  Ser Cys Pro Pro Asn Thr Ile Leu Lys Ala His Gln Pro Tyr Gly Val
323      370             375             380
325  Gln Ala Cys Val Pro Cys Gly Pro Gly Thr Lys Asn Asn Lys Ile His
326  385             390             395             400
328  Ser Leu Cys Tyr Asn Asp Cys Thr Phe Ser Arg Asn Thr Pro Thr Arg
329          405             410             415
331  Thr Phe Asn Tyr Asn Phe Ser Ala Leu Ala Asn Thr Val Thr Leu Ala
332          420             425             430
334  Gly Gly Pro Ser Phe Thr Ser Lys Gly Leu Lys Tyr Phe His His Phe
335          435             440             445
337  Thr Leu Ser Leu Cys Gly Asn Gln Gly Arg Lys Met Ser Val Cys Thr
338      450             455             460
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VERIFICATION SUMMARY
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Input Set : **A:\PF511P1 seqlisting.txt**
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L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
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L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
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L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48

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L:2452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50